

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/777,317

DATE: 06/26/2001  
TIME: 02:29:14

INPUT SET: S36571.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4 (i) APPLICANT: Gossen, Manfred  
5 Bujard, Hermann  
6 Salfeld, Jochen  
7 Voss, Jeffrey  
8  
9 (ii) TITLE OF INVENTION: Methods for Regulating Gene Expression  
10 (iii) NUMBER OF SEQUENCES: 10  
11 (iv) CORRESPONDENCE ADDRESS:  
12  
13 (A) ADDRESSEE: Lahive & Cockfield  
14 (B) STREET: 60 State Street, Suite 510  
15 (C) CITY: Boston  
16 (D) STATE: Massachusetts  
17 (E) COUNTRY: USA  
18 (F) ZIP: 02109-1875  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: ASCII text  
24  
25 (vi) CURRENT APPLICATION DATA:  
26 (A) APPLICATION NUMBER: 09/777,317  
27 (B) FILING DATE:  
28 (C) CLASSIFICATION:  
29 (vii) PRIOR APPLICATION DATA:  
30 (A) APPLICATION NUMBER: 08/479,306  
31 (B) FILING DATE:  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: 08/076,327  
34 (B) FILING DATE: 14-JUN-1993  
35 (viii) ATTORNEY/AGENT INFORMATION:  
36 (A) NAME: Giulio A. DeConti, Jr.  
37 (B) REGISTRATION NUMBER: 31,503  
38 (C) REFERENCE/DOCKET NUMBER: BBI-013CP3  
39  
40 (ix) TELECOMMUNICATION INFORMATION:  
41 (A) TELEPHONE: (617) 227-7400  
42 (B) TELEFAX: (617) 227-5941  
43  
44 (2) INFORMATION FOR SEQ ID NO:1:  
45  
46 (i) SEQUENCE CHARACTERISTICS:

ENTERED

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/777,317*

 DATE: 06/26/2001  
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47 (A) LENGTH: 1008 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: DNA (genomic)
53
54 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Herpes Simplex Virus
56 (B) STRAIN: K12, KOS
57
58 (vii) IMMEDIATE SOURCE:
59 (B) CLONE: tTA transactivator
60
61 (ix) FEATURE:
62 (A) NAME/KEY: exon
63 (B) LOCATION: 1..1008
64
65 (ix) FEATURE:
66 (A) NAME/KEY: mRNA
67 (B) LOCATION: 1..1008
68
69 (ix) FEATURE:
70 (A) NAME/KEY: misc. binding
71 (B) LOCATION: 1..207
72
73 (ix) FEATURE:
74 (A) NAME/KEY: misc. binding
75 (B) LOCATION: 208..335
76
77 (ix) FEATURE:
78 (A) NAME/KEY: CDS
79 (B) LOCATION: 1..1005
80
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
82 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG      48
83 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
84   1               5               10               15
85
86 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG      96
87 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
88           20               25               30
89
90 AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG      144
91 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
92           35               40               45
93
94 CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT      192
95 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
96           50               55               60
97
98 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT      240
99 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
    
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	65	70	75	80	
100					
101					
102	AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA				288
103	Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly				
104		85	90	95	
105					
106	GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT				336
107	Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr				
108		100	105	110	
109					
110	CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG				384
111	Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu				
112		115	120	125	
113					
114	AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC				432
115	Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys				
116		130	135	140	
117					
118	GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA				480
119	Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr				
120		145	150	155	160
121					
122	CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA				528
123	Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu				
124		165	170	175	
125					
126	TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG				576
127	Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu				
128		180	185	190	
129					
130	ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG				624
131	Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala				
132		195	200	205	
133					
134	TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC				672
135	Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly				
136		210	215	220	
137					
138	CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG				720
139	Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala				
140		225	230	235	240
141					
142	GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG				768
143	Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser				
144		245	250	255	
145					
146	ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC				816
147	Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp				
148		260	265	270	
149					
150	GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT				864
151	Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp				
152		275	280	285	

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153																			
154	CTG	GAC	ATG	TTC	GGG	GAC	GGG	GAT	TCC	CCG	GGT	CCG	GGA	TTT	ACC	CCC		912	
155	Leu	Asp	Met	Leu	Gly	Asp	Gly	Asp	Ser	Pro	Gly	Pro	Gly	Phe	Thr	Pro			
156		290					295					300							
157																			
158	CAC	GAC	TCC	GCC	CCC	TAC	GGC	GCT	CTG	GAT	ATG	GCC	GAC	TTC	GAG	TTT		960	
159	His	Asp	Ser	Ala	Pro	Tyr	Gly	Ala	Leu	Asp	Met	Ala	Asp	Phe	Glu	Phe			
160		305				310					315					320			
161																			
162	GAG	CAG	ATG	TTT	ACC	GAT	CCC	CTT	GGA	ATT	GAC	GAG	TAC	GGT	GGG	TAG		1008	
163	Glu	Gln	Met	Phe	Thr	Asp	Pro	Leu	Gly	Ile	Asp	Glu	Tyr	Gly	Gly				
164					325					330					335				
165																			
166	(2)	INFORMATION FOR SEQ ID NO:2:																	
167	(i)	SEQUENCE CHARACTERISTICS:																	
168	(A)	LENGTH: 335 amino acids																	
169	(B)	TYPE: amino acid																	
170	(D)	TOPOLOGY: linear																	
171	(ii)	MOLECULE TYPE: protein																	
172	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:2:																	
173	Met	Ser	Arg	Leu	Asp	Lys	Ser	Lys	Val	Ile	Asn	Ser	Ala	Leu	Glu	Leu			
174	1				5					10					15				
175																			
176	Leu	Asn	Glu	Val	Gly	Ile	Glu	Gly	Leu	Thr	Thr	Arg	Lys	Leu	Ala	Gln			
177				20					25					30					
178																			
179	Lys	Leu	Gly	Val	Glu	Gln	Pro	Thr	Leu	Tyr	Trp	His	Val	Lys	Asn	Lys			
180			35					40					45						
181																			
182	Arg	Ala	Leu	Leu	Asp	Ala	Leu	Ala	Ile	Glu	Met	Leu	Asp	Arg	His	His			
183		50					55					60							
184																			
185	Thr	His	Phe	Cys	Pro	Leu	Glu	Gly	Glu	Ser	Trp	Gln	Asp	Phe	Leu	Arg			
186	65					70					75					80			
187																			
188	Asn	Lys	Ala	Lys	Ser	Phe													

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206 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
207           180                      185                      190
208
209 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
210           195                      200                      205
211
212 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
213           210                      215                      220
214
215 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
216 225                      230                      235                      240
217
218 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
219           245                      250                      255
220
221 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
222           260                      265                      270
223
224 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
225           275                      280                      285
226
227 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
228 290                      295                      300
229
230 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
231 305                      310                      315                      320
232
233 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
234           325                      330                      335
235
236

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237 (2) INFORMATION FOR SEQ ID NO:3:
238 (i) SEQUENCE CHARACTERISTICS:
239 (A) LENGTH: 894 base pairs
240 (B) TYPE: nucleic acid
241 (C) STRANDEDNESS: double
242 (D) TOPOLOGY: linear
243
244 (ii) MOLECULE TYPE: DNA (genomic)
245
246 (vi) ORIGINAL SOURCE:
247 (A) ORGANISM: Herpes Simplex Virus
248 (B) STRAIN: K12, KOS
249 (C) INDIVIDUAL ISOLATE: tTAS transactivator
250
251 (ix) FEATURE:
252 (A) NAME/KEY: exon
253 (B) LOCATION: 1..894
254
255 (ix) FEATURE:
256 (A) NAME/KEY: mRNA
257 (B) LOCATION: 1..894
258

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